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Figure 1 - Healthy Nucleus Pulposus Tissue

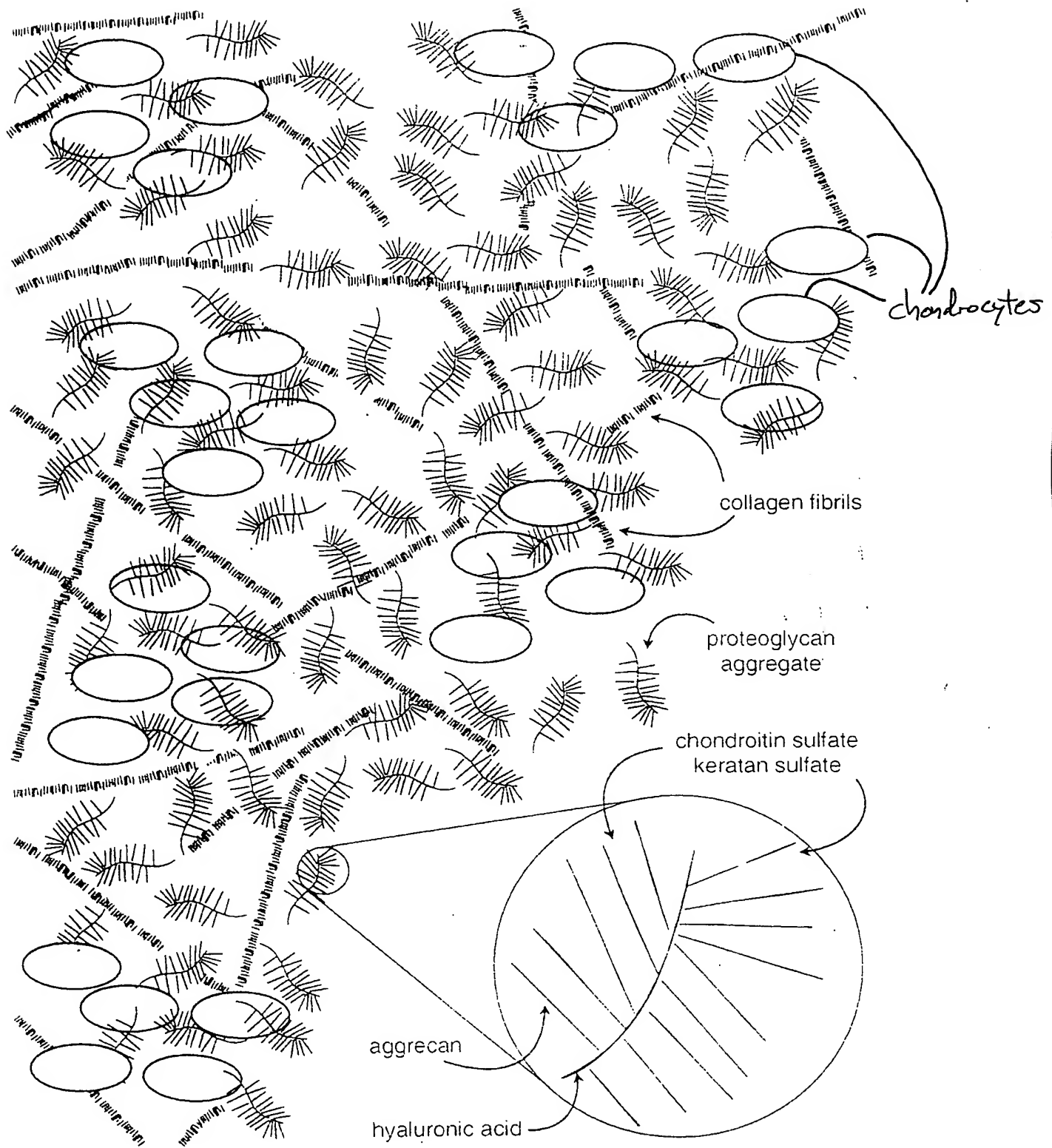


Figure 2: Cross-linked Matrix

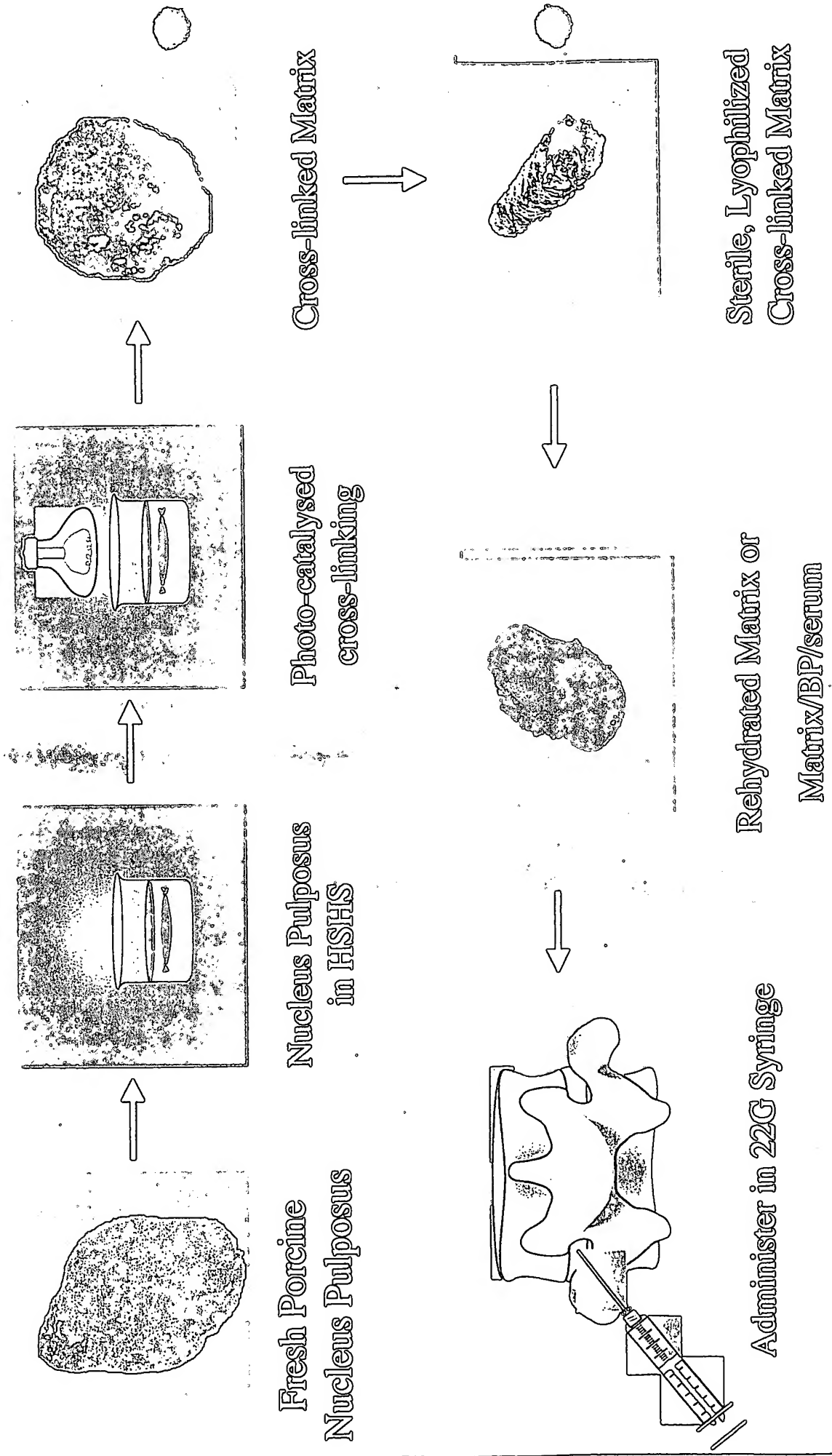


Figure 3



A B

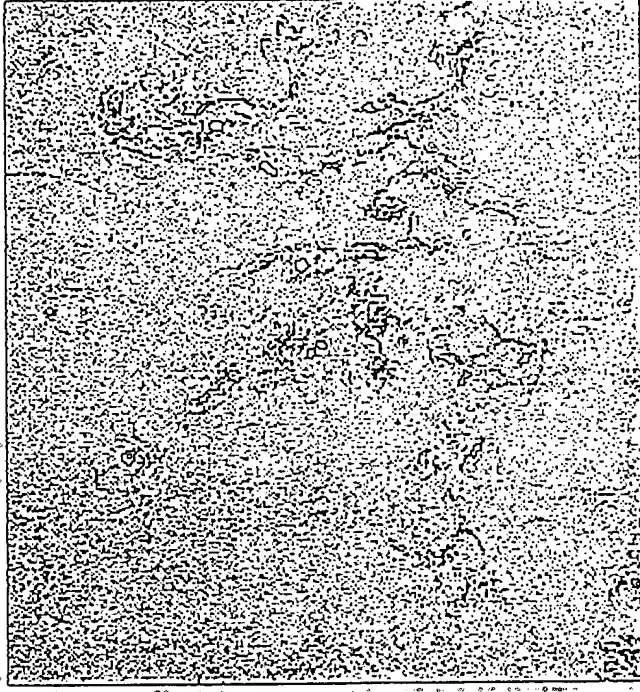
- Lane A: Non cross-linked control shows substantial protein extraction
- Lane B: Cross-linked matrix demonstrates reduced protein extraction

Figure 4: Comparison of Fresh Porcine Nucleus Pulposus versus Cross-linked Matrix



Fresh Nucleus Pulposus

- round, nucleated chondrocytes
- intact pericellular matrix "nests"



Cross-linked Matrix

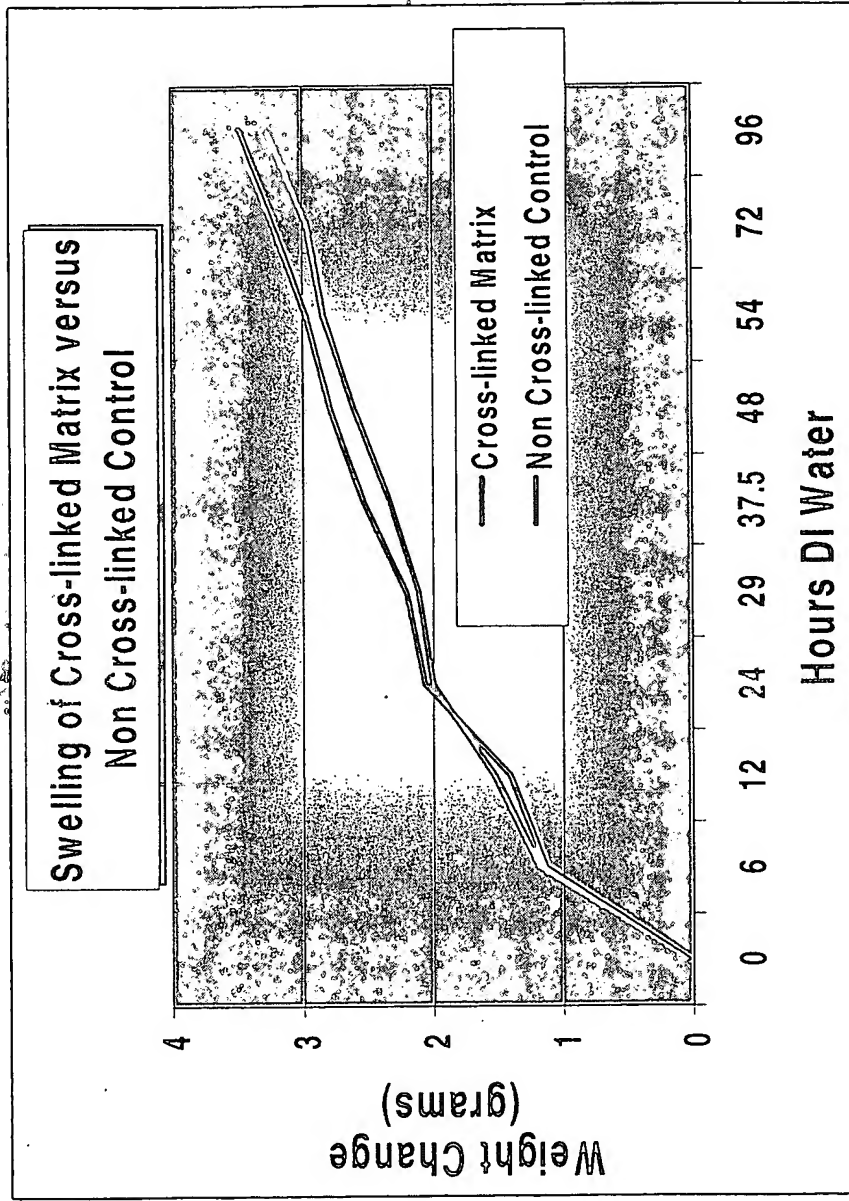
- disrupted, crenated cell fragments
- minimal cell membrane material
- further isopropanol sterilization

Figure 5



- Lane A: Pepsin digests of non cross-linked control react with Type III collagen antibodies
- Lane B: Pepsin digests of cross-linked matrix does not react with Type III collagen antibodies

Figure 6



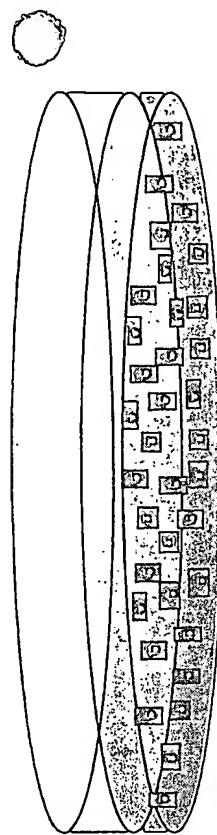
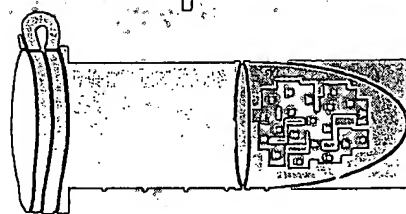
•Cross-linked matrix retains 95% hydraulic capacity

Figure 7: Growth and Proliferation of Disc cells into Cross-linked Matrix

Culture Expansion

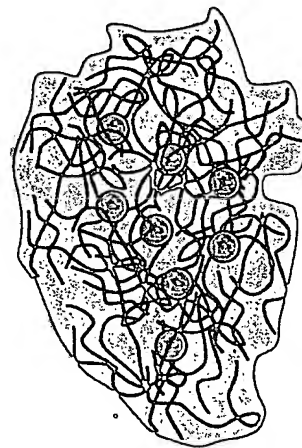
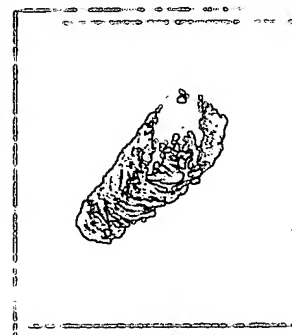
Cell Isolation

Sterile nucleus pulposus
from sheep spine;
enzymatic digestion for
cell isolation



Disc Cell Culture in
Cross-linked Matrix/BP

Cross-linked matrix/BP



Cross-linked
matrix
seeded with
disc cells &
stained with
phalloidin

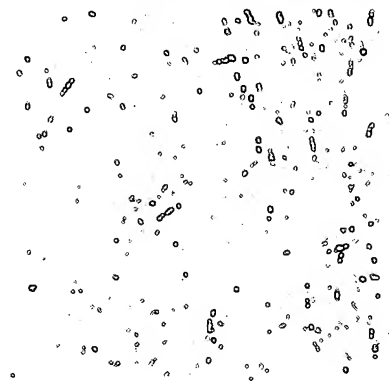
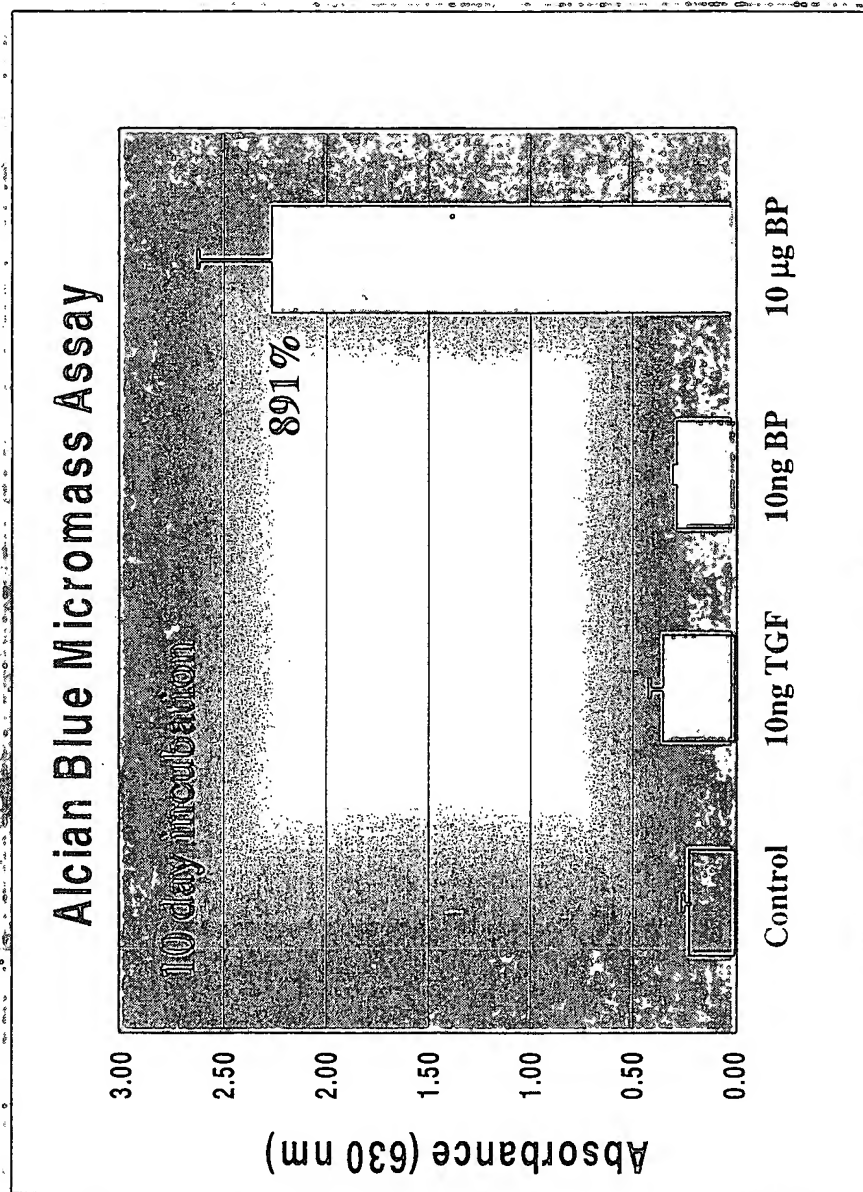


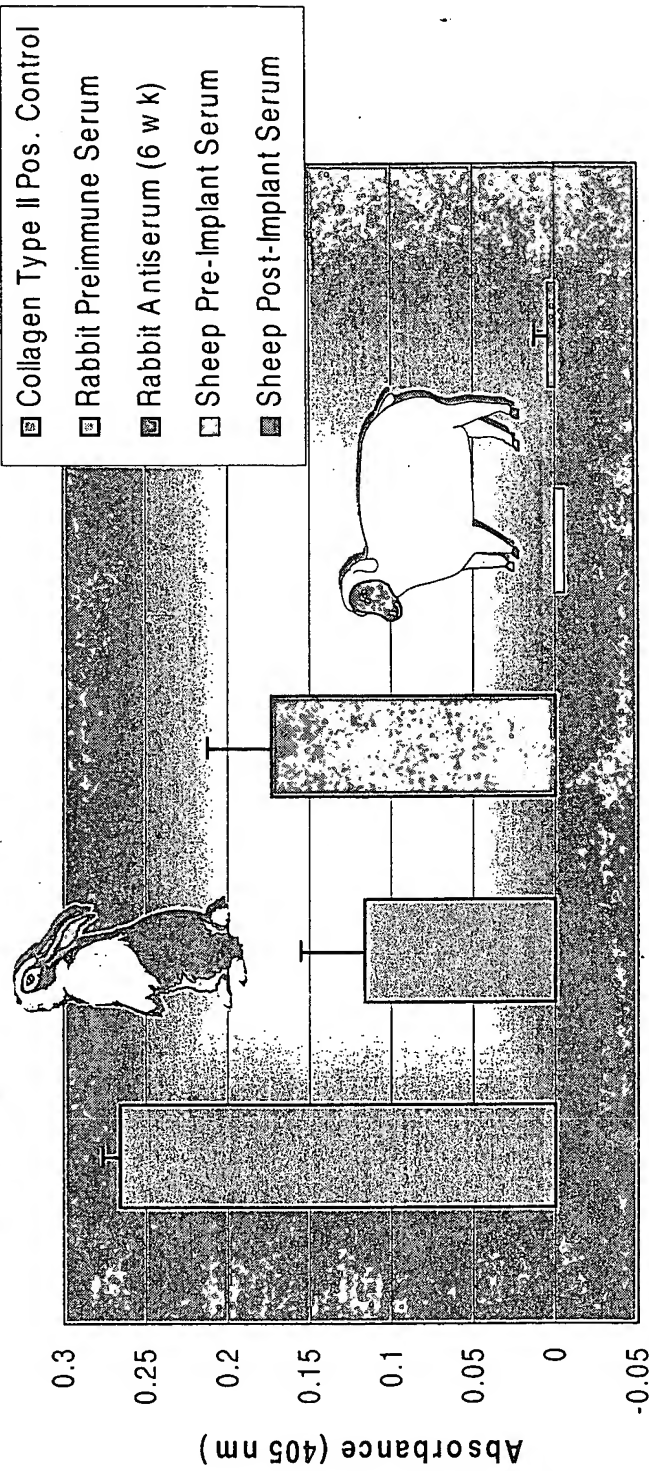
Figure 8: Growth Factor Stimulation of Matrix Synthesis



• Significant stimulation of matrix production only at µg BP concentrations

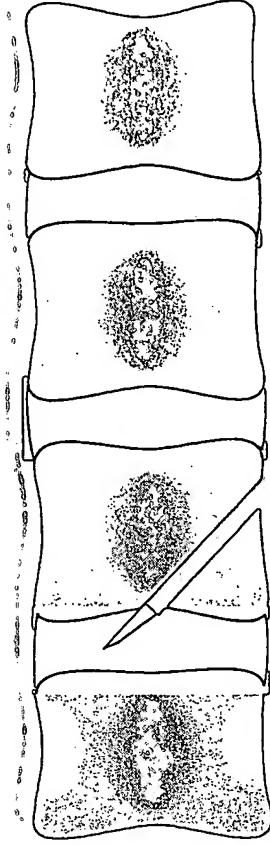
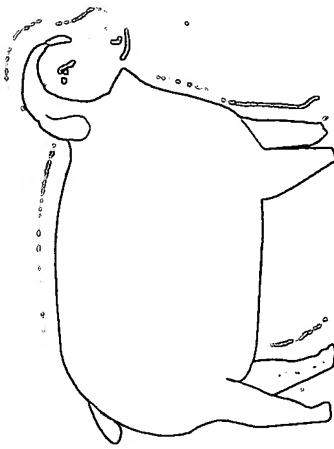
Fig 2. Cross-linked Matrix Immunization

ELISA Analysis of Cross-linked Matrix



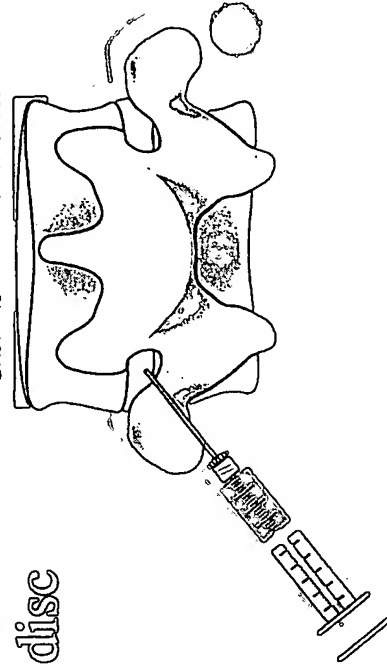
- Low antibody titers to cross-linked matrix in rabbit immunizations
- No serum antibodies to cross-linked matrix *in vivo* (1st sheep)

1st operation: annulus stabs to
create two degenerative discs



Wait 2 months

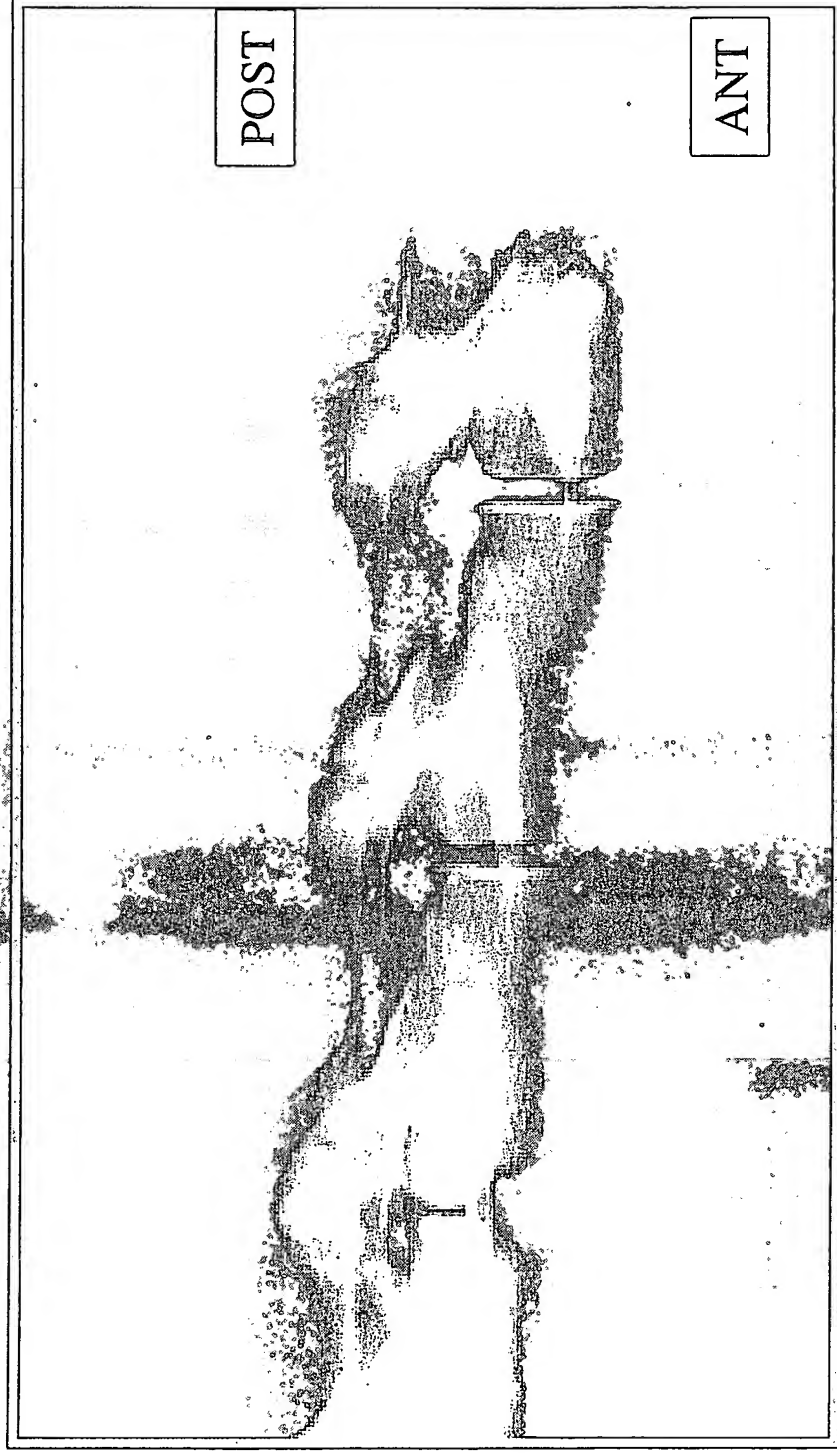
2nd operation: Cross-linked matrix/BP
gel treatment injection to one disc



- Histomorphometry
- MRI/radiographs
- Immune response

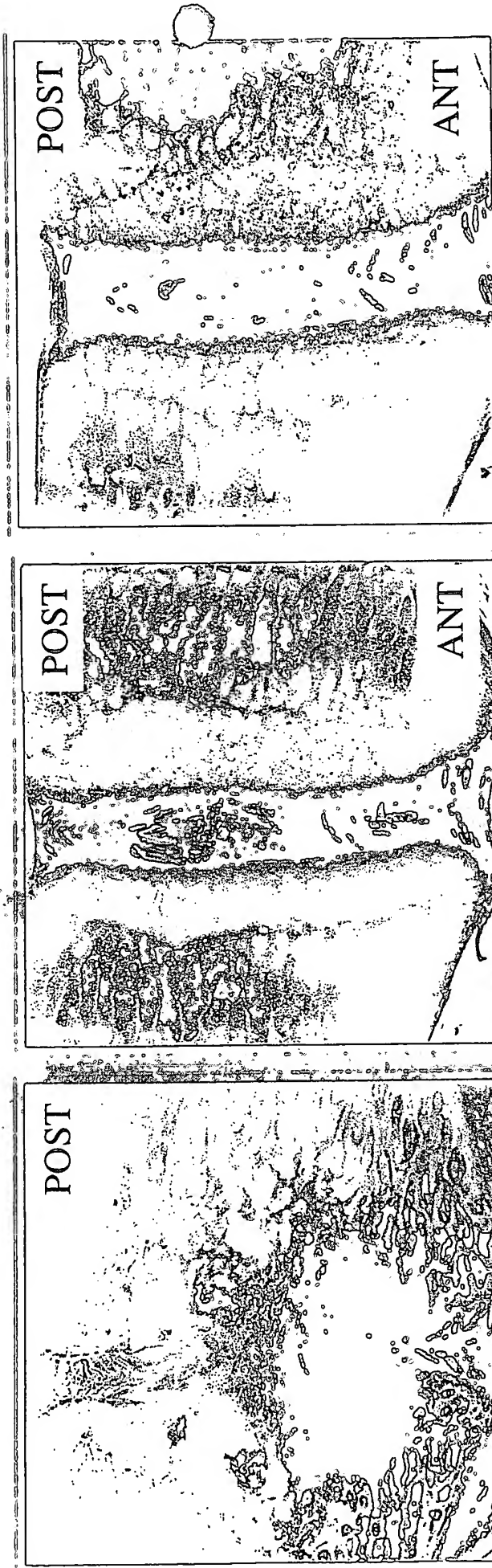
Sacrifice: 2, 4, and 6 months

*Figure 11: Radiograph-Pilot Study #1
2 Months Post Injection (Cross-linked matrix/BP)*



- Treated and Control discs: normal size and appearance of disc structures
- Untreated disc: disjunct endplates, bone resorption and remodeling

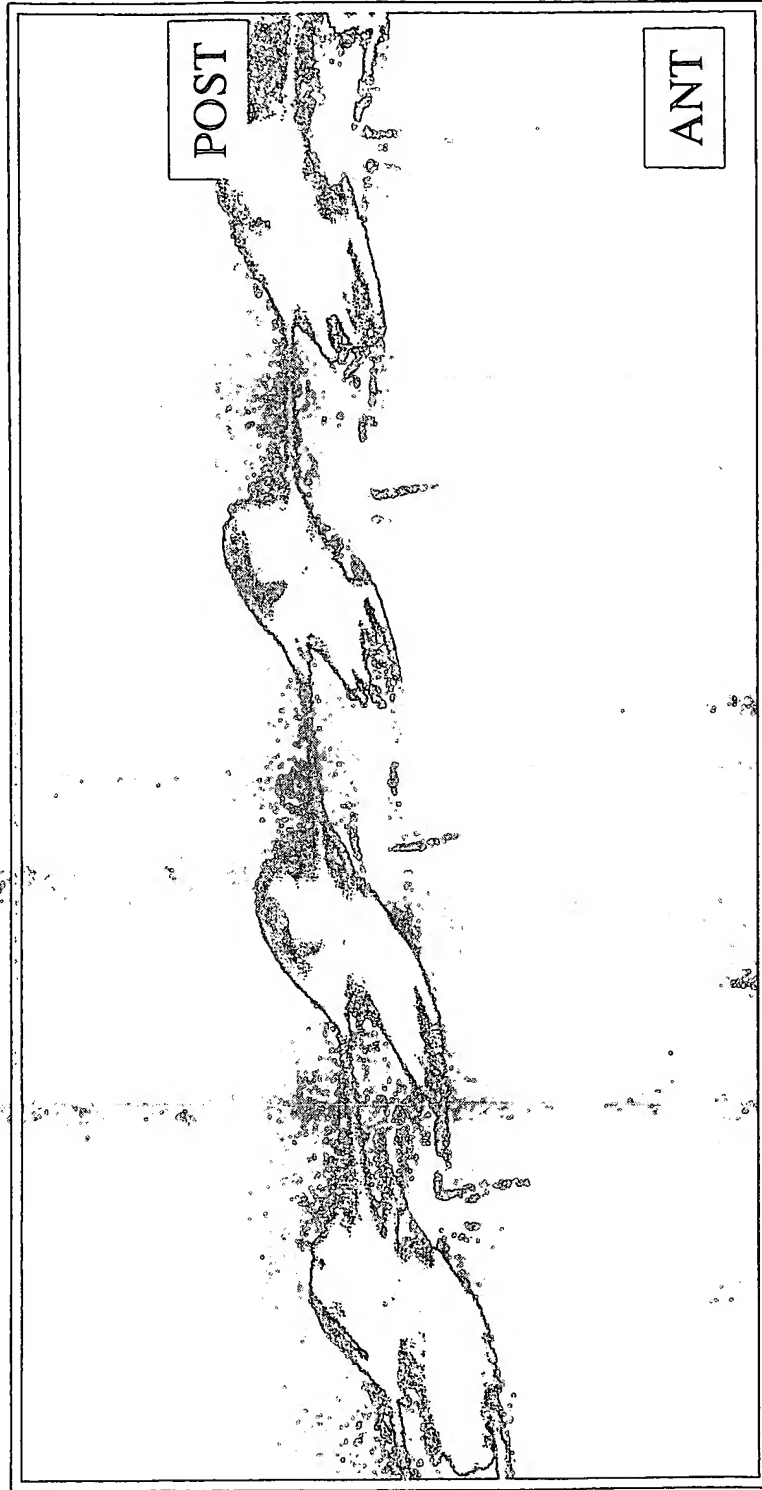
Figure 12: Histology- Pilot Study #1



2 Months Post-Injection

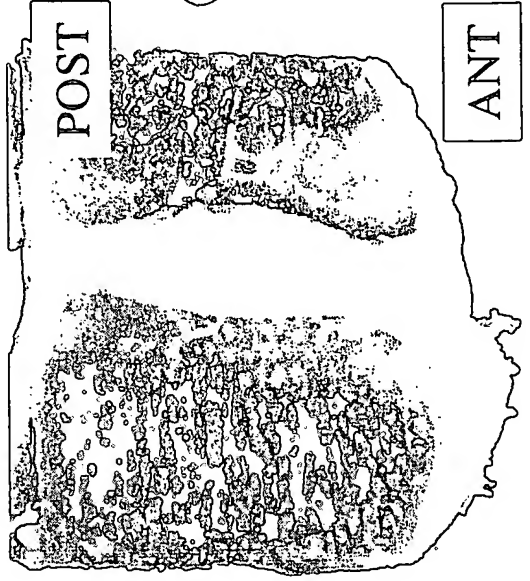
- Untreated disc exhibits extensive degeneration
- Cross-linked matrix/BP-treated disc retains normal structures similar to Control disc

*Figure 13: Radiograph- Pilot Study #1
4 Months Post Injection (Cross-linked matrix/BP)*



- No apparent radiographic differences between discs in 4 month sheep.

Figure 14: Histology- Pilot Study #1



4 Months Post-Injection

- Untreated disc exhibits degenerative changes
- Cross-linked matrix/BIP-treated disc similar to control disc: normal gelatinous nucleus, regular annulus, intact endplates

Figure 15: Growth Factor Stimulation of Type II Collagen & Chondroitin-6-Sulfate Synthesis

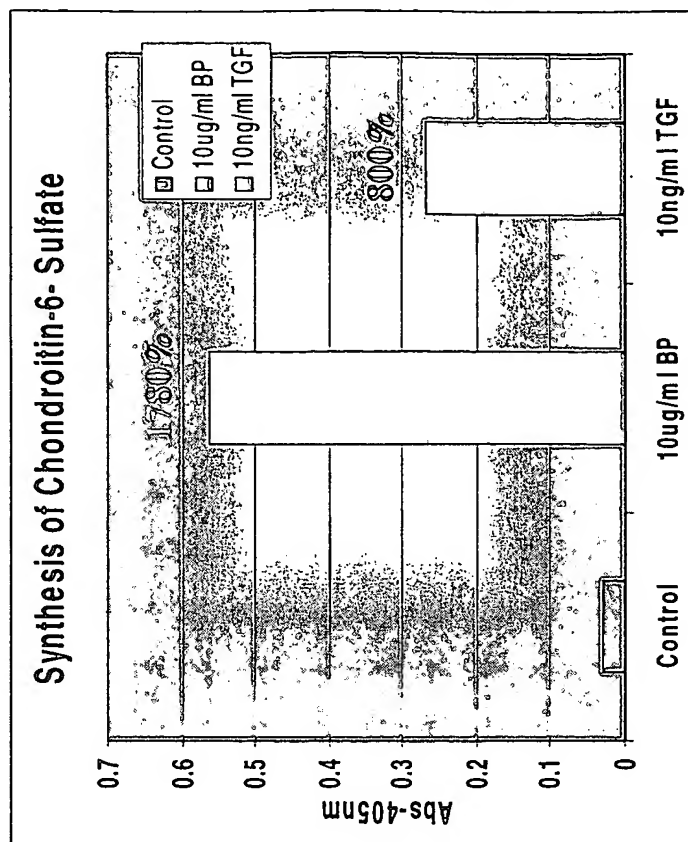
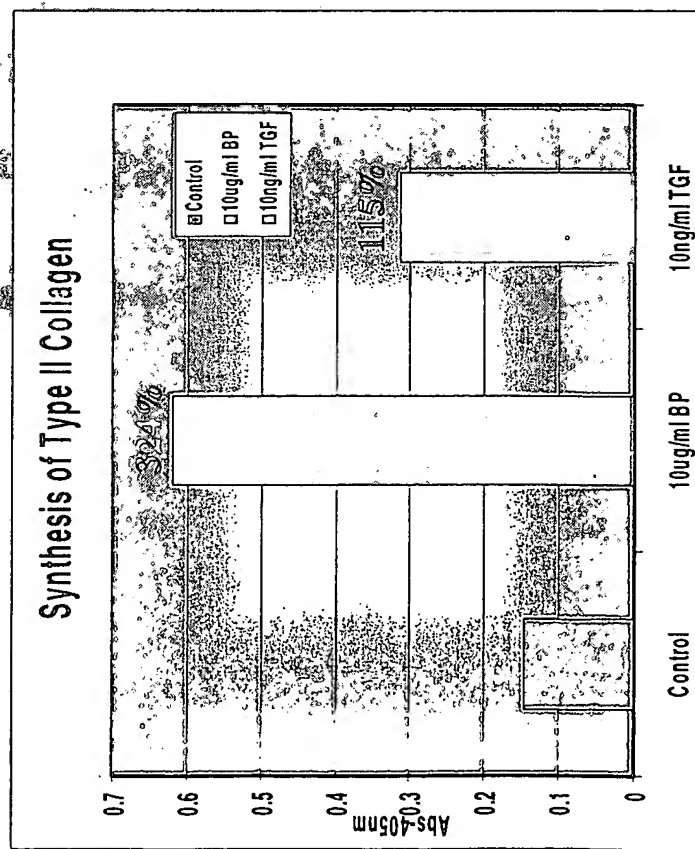


Figure 16: Growth Factor Stimulation of Proteoglycan Synthesis in Human Intervertebral Disc Nucleus Pulposus Cells

Figure 16a

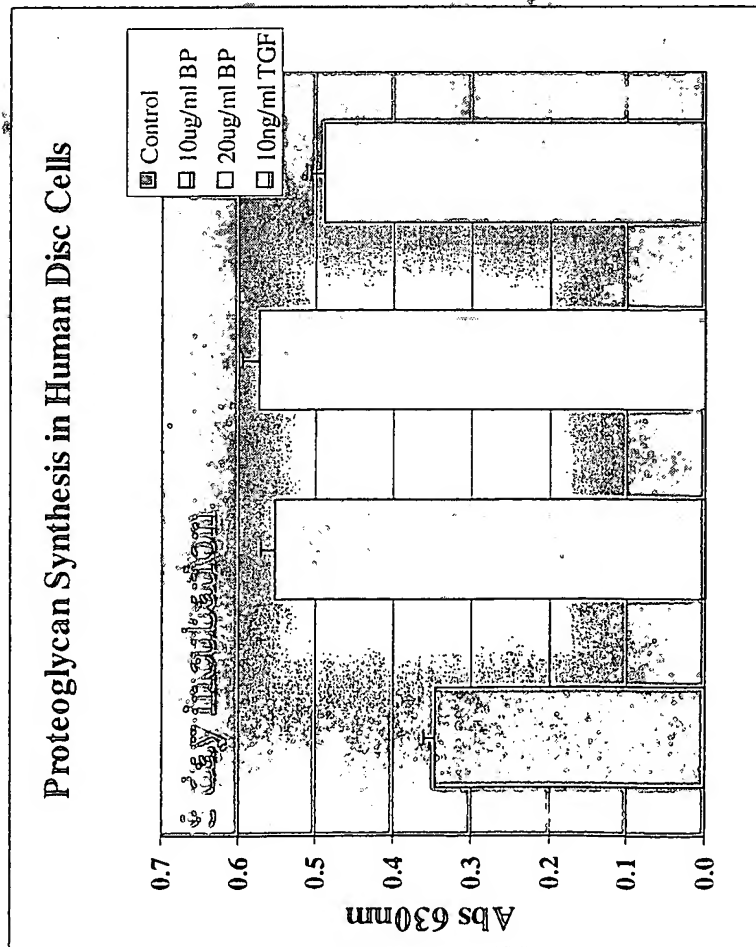
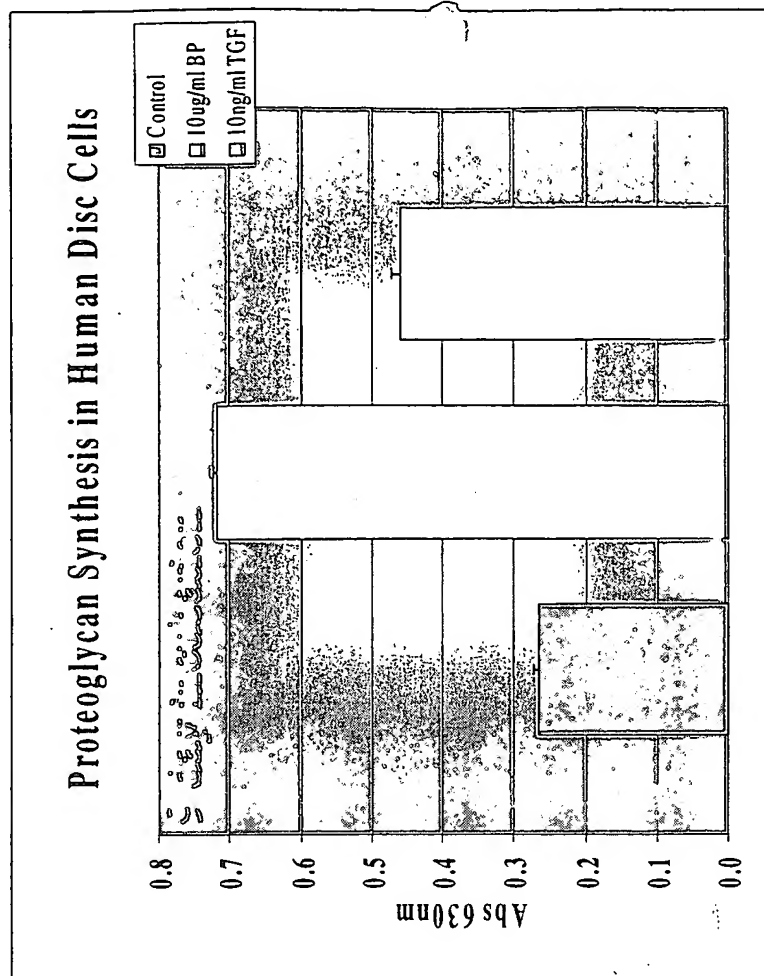


Figure 16b



*Figure 17: Growth Factor Stimulation of
Proteoglycan Synthesis in Baboon Intervertebral
Disc Nucleus Pulposus Cells*

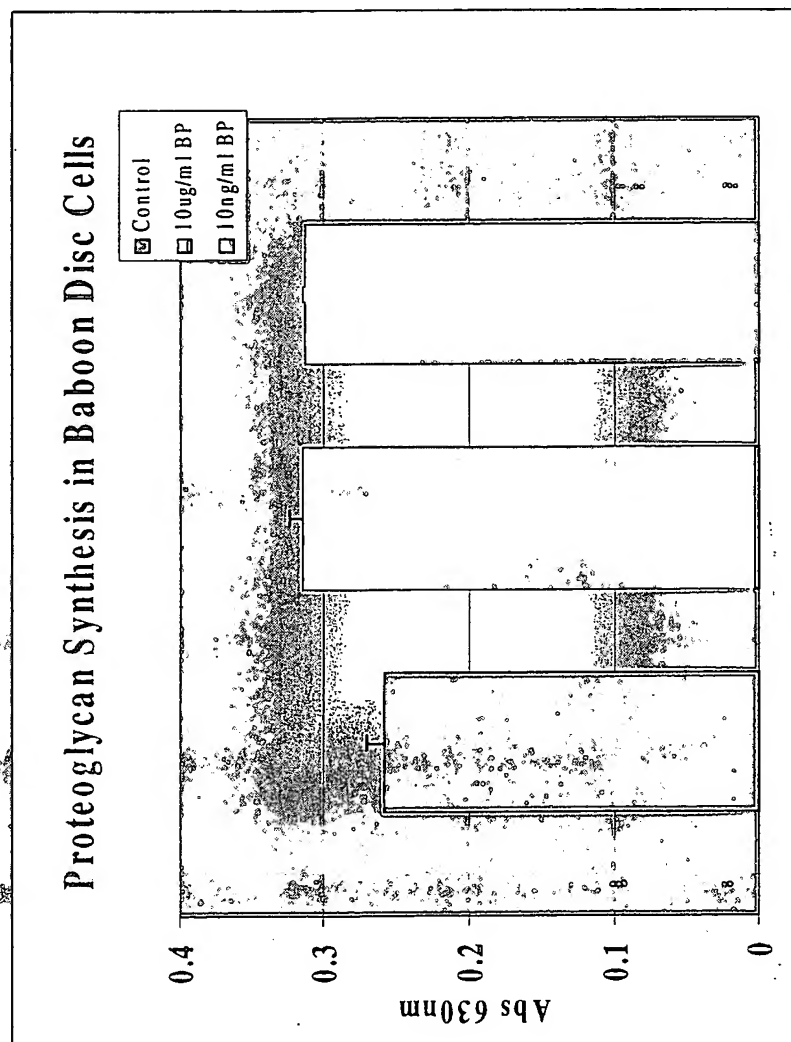


FIGURE 18

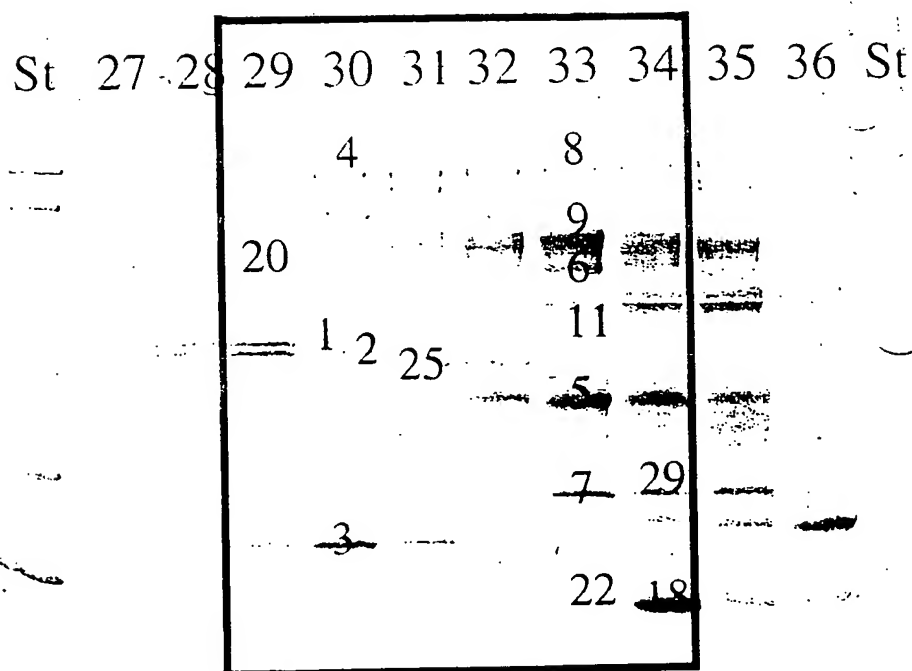
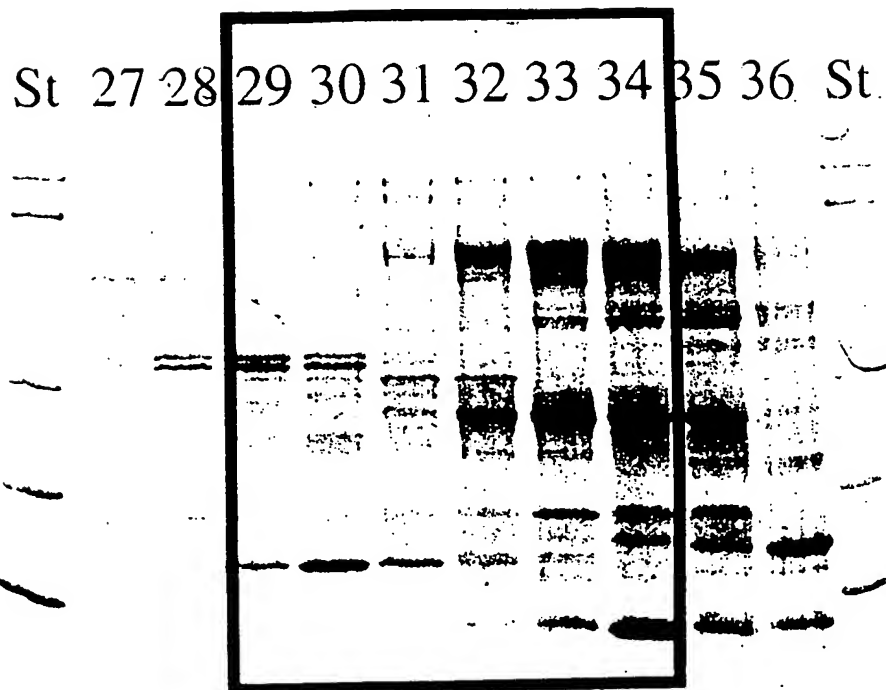


FIGURE 19



| Band No. | Identity |
|----------|--------------------------------------|
| 1 | histone H1.c |
| 2 | histone H1.c |
| 3 | ribosomal protein RS20 |
| 4 | similar to ribosomal protein LORP |
| 5 | BMP-3 |
| 6 | α 2 macroglobulin RAP & BMP-3 |
| 7 | similar to ribosomal protein LORP |
| 8 | BMP-3 |
| 9 | BMP-3 |
| 11 | ribosomal protein RL6 & BMP-3 |
| 18 | TGF- β 2/SPP24 |
| 20 | Factor H |
| 22 | TGF- β 2 |
| 25 | BMP-3 & H1.x |
| 29 | BMP-3 & ribosomal protein RL32 |

FIGURE 20

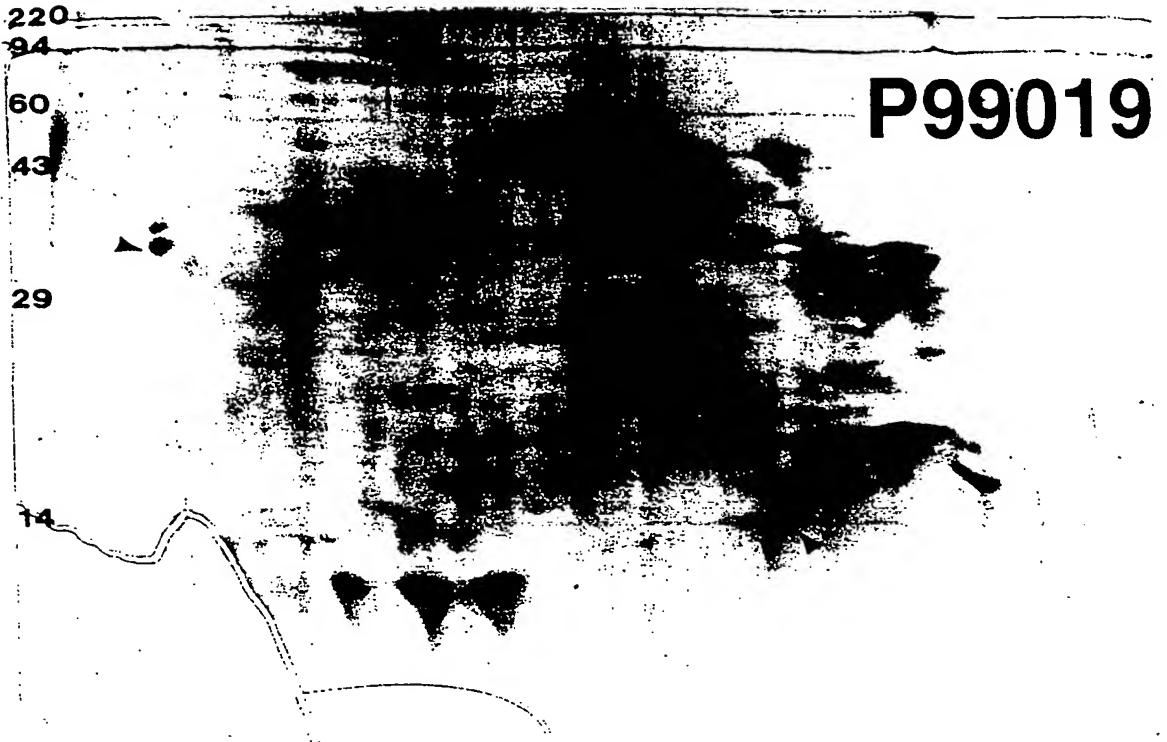
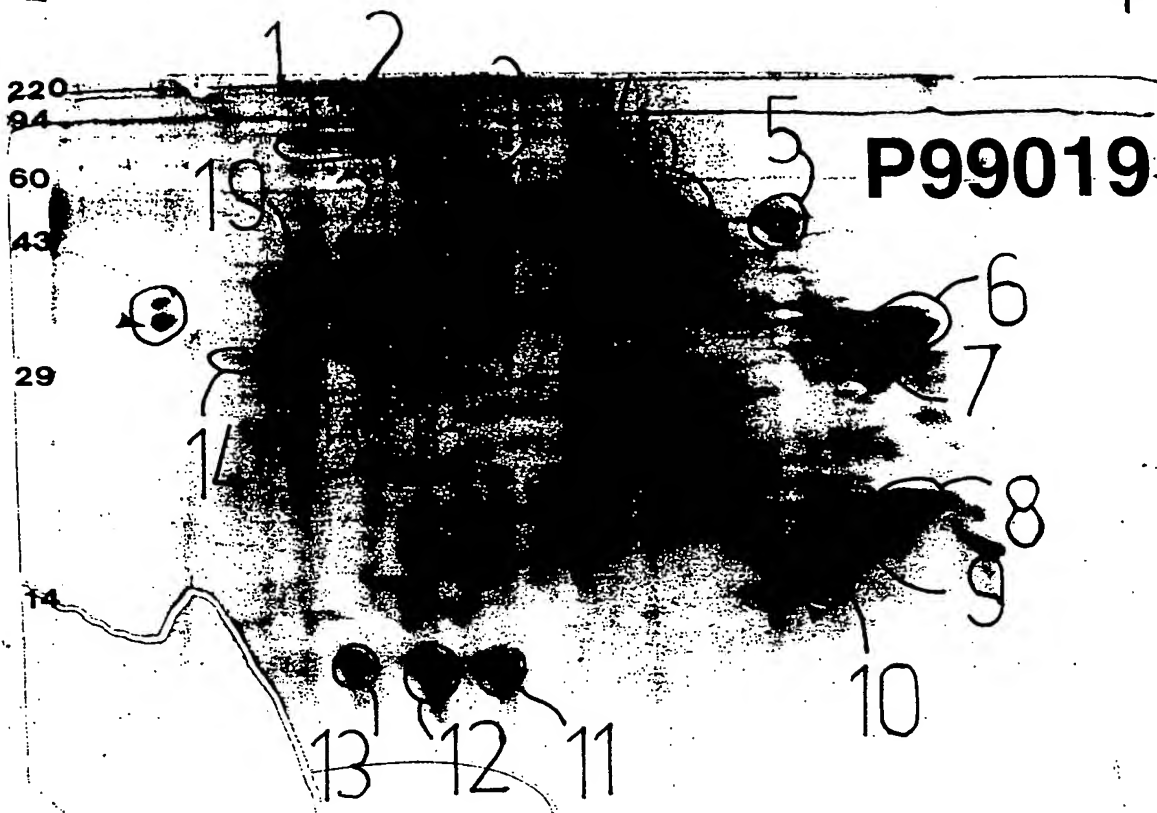


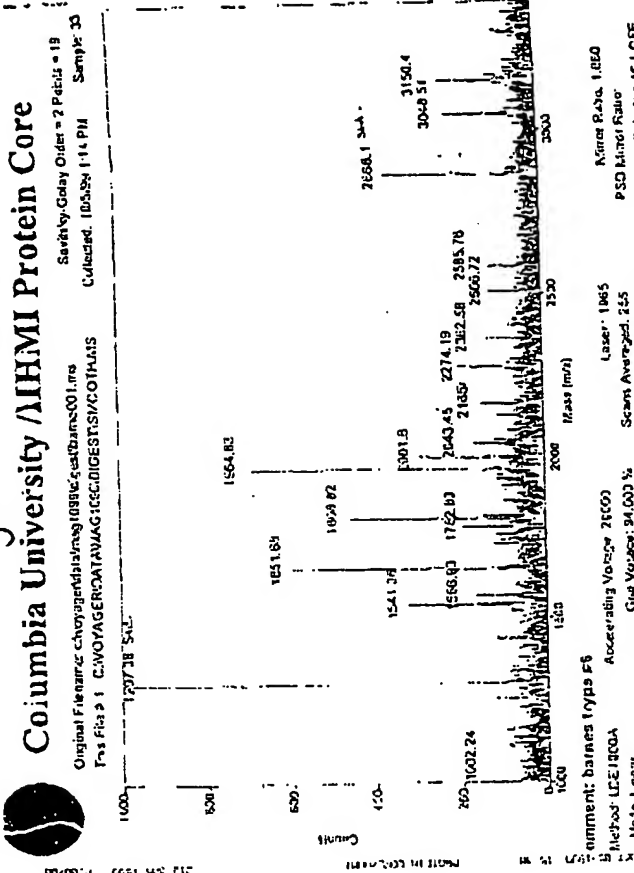
FIGURE 21



| No. | Identity | No. | Identity |
|-----|-------------|-----|----------------------|
| 1 | Factor XIII | 11 | TGF- β 2/SPP24 |
| 2 | LORP | 12 | SPP24 |
| 3 | LORP | 12 | TGF- β 2/SPP24 |
| 4 | | 14 | lysyl oxidase |
| 5 | RL3 | 15 | lysyl oxidase |
| 6 | | 16 | lysyl oxidase |
| 7 | | 17 | lysyl oxidase |
| 8 | | 18 | BMP-3 |
| 9 | | 19 | cathepsin L |
| 10 | | 20 | |
| | | 21 | RS3a |

FIGURE 22

Figure 23 F (Band 6)



Columbia University / HHMI Protein Core

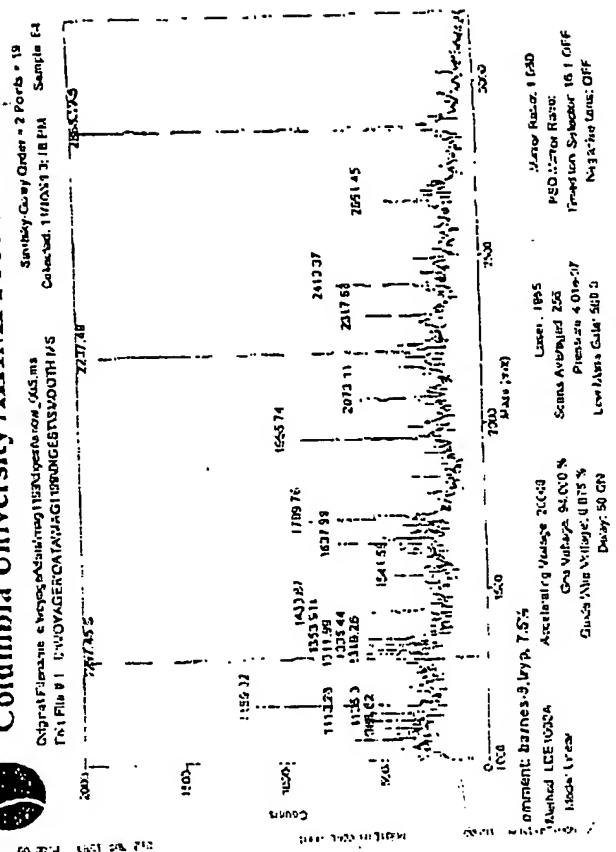
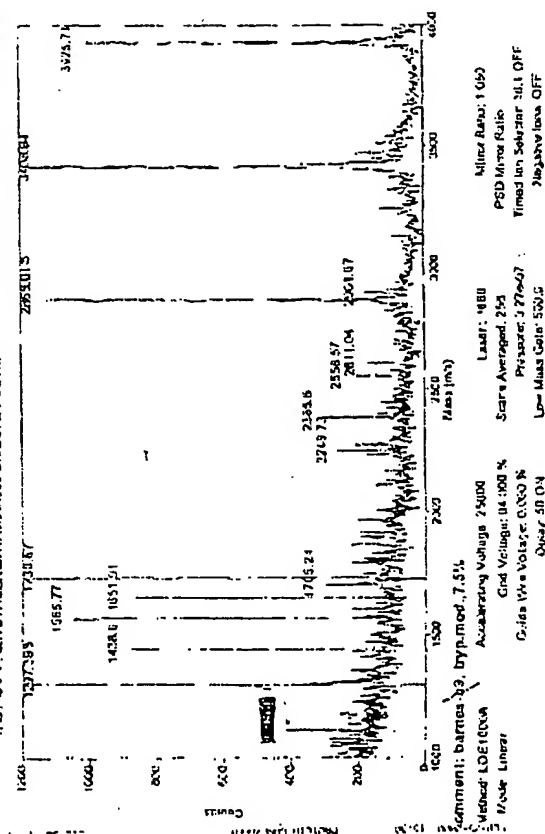


Figure 23H (Band 8)

Figure 23 J (Band 11)

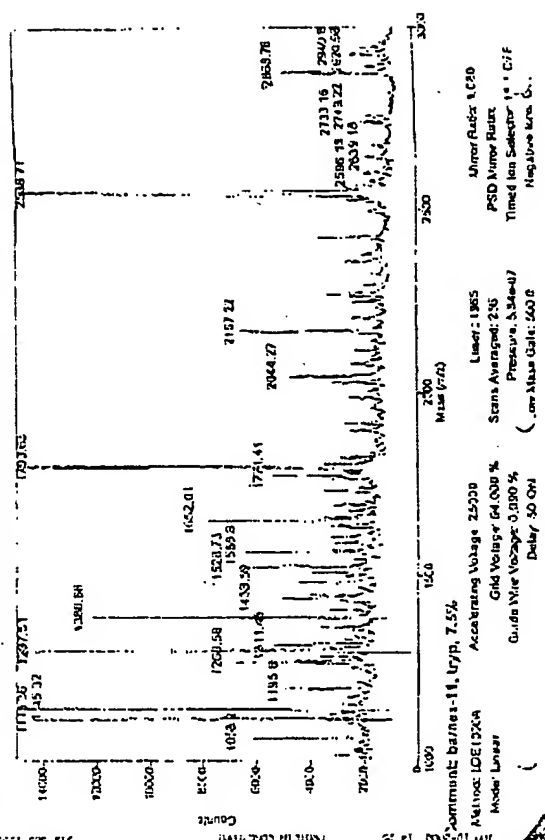
Columbia University / FHM Protein Core

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 Swathby-Gidday Order = 2 Points = 10



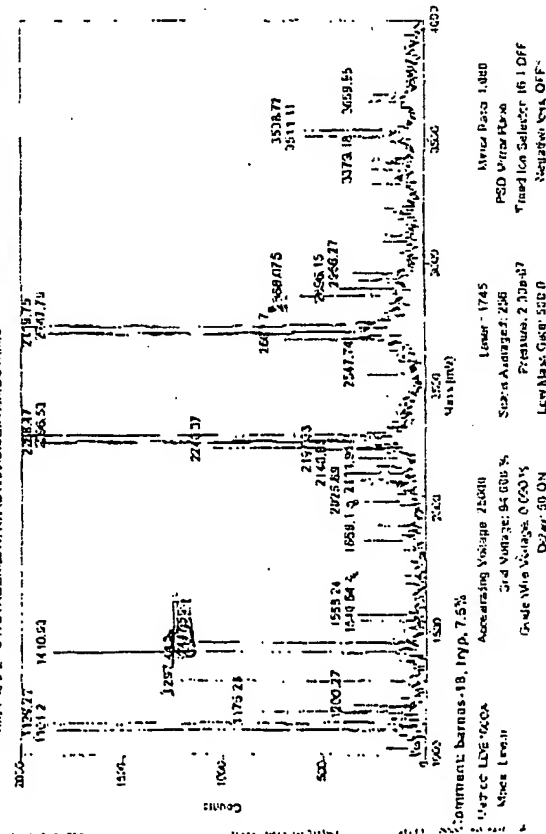
Columbia University /FHM1 Protein Core

Original File Name: C:\wp3\cf\d3\cf\mg1289\digest\mod004.ms
File # 2: C:\VOLUME\DATA\MAG1289\DIGEST\MOD0011.MS
Sample: Gaby O-21 # 2 Purist # 13
Collected: 12/15/92 1:49 PM Sample # 4



Columbia University / HHMI Protein Core

Original filename: C:\cra\2016-03-08\mmsj125b7v4e\CurveC05.mlx
This file is 2 C:\VOYAGEONDATA\AGI\TUP01ENTRITEMDO\THIS
Sample: 13 Collected: 02MAR2016 4:41 PM Sample: 13
Surveying Order = 2 Plot: 19



Columbia University / HHMI Protein Core

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Contacted 10/20/2008 PM Sample #3
Serial# Galaxy Order = 2 PCEMS = 19

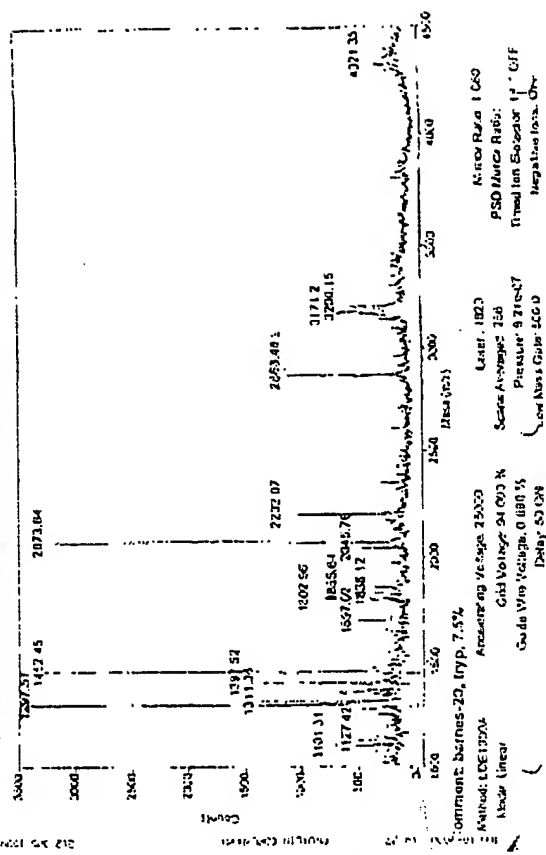


Figure 23 K (Band 18)

Figure 23 L (Band 20)

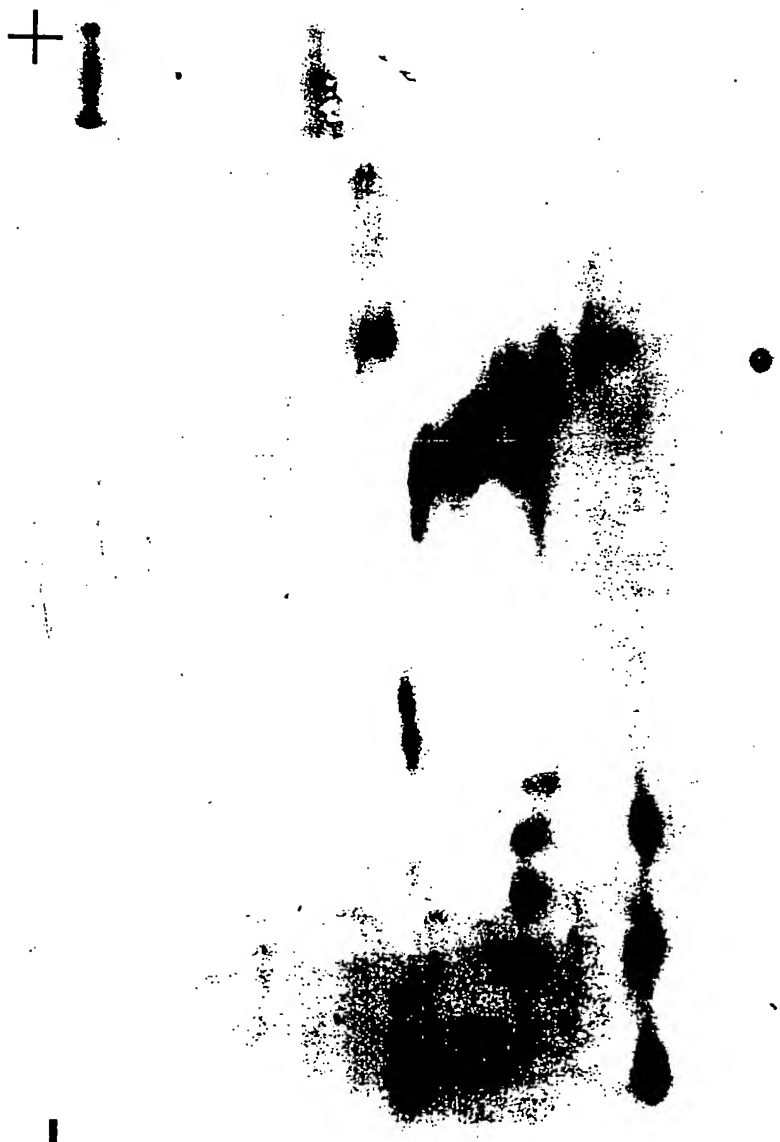


FIGURE 24

+

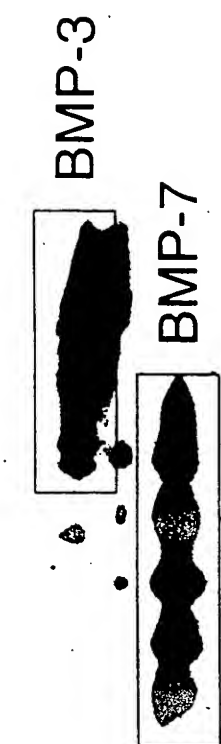


FIGURE 25B



FIGURE 25D

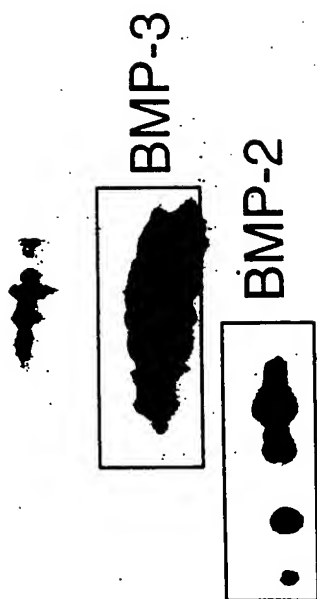


FIGURE 25A

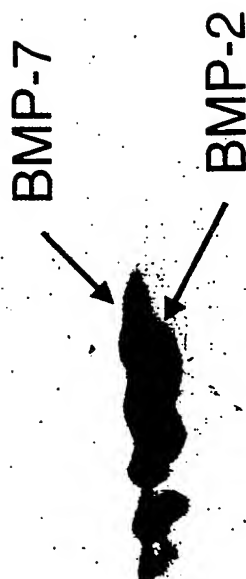


FIGURE 25C

FIGURE 26

29 30 31 32 33 34 35 36 37 38

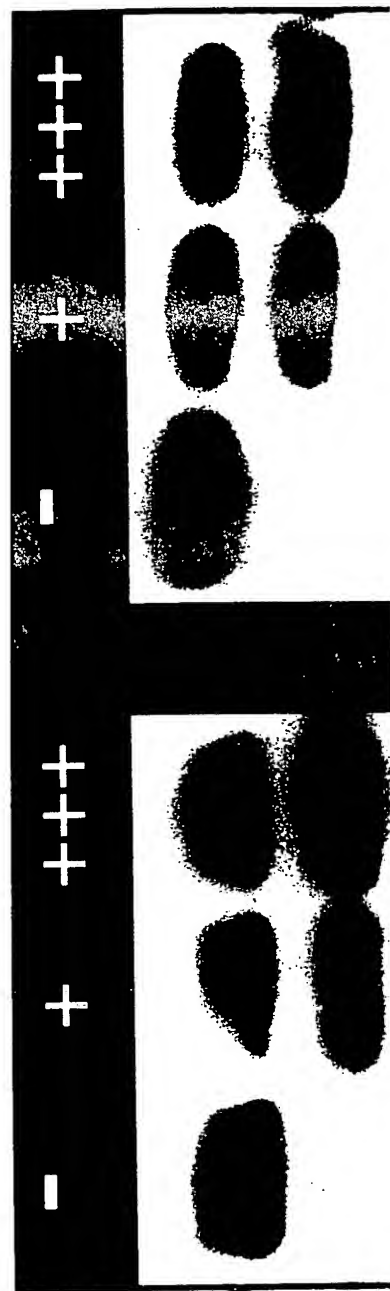
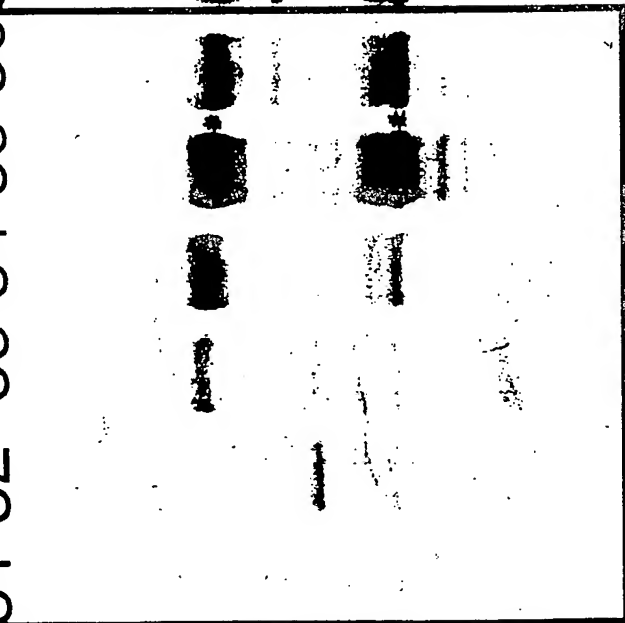


FIGURE 27

FIGURE 28

FIGURE 29A

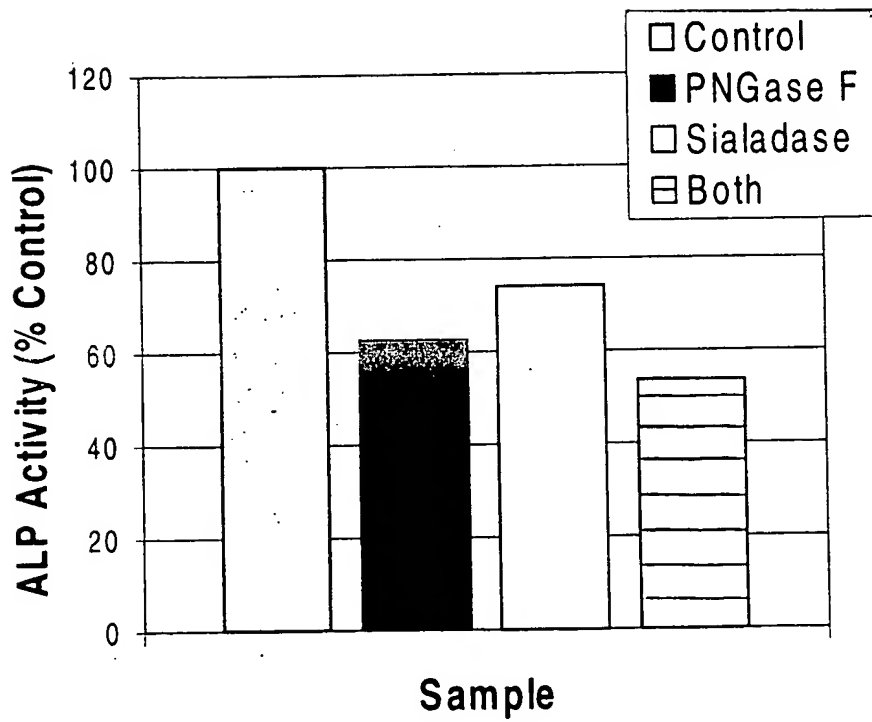
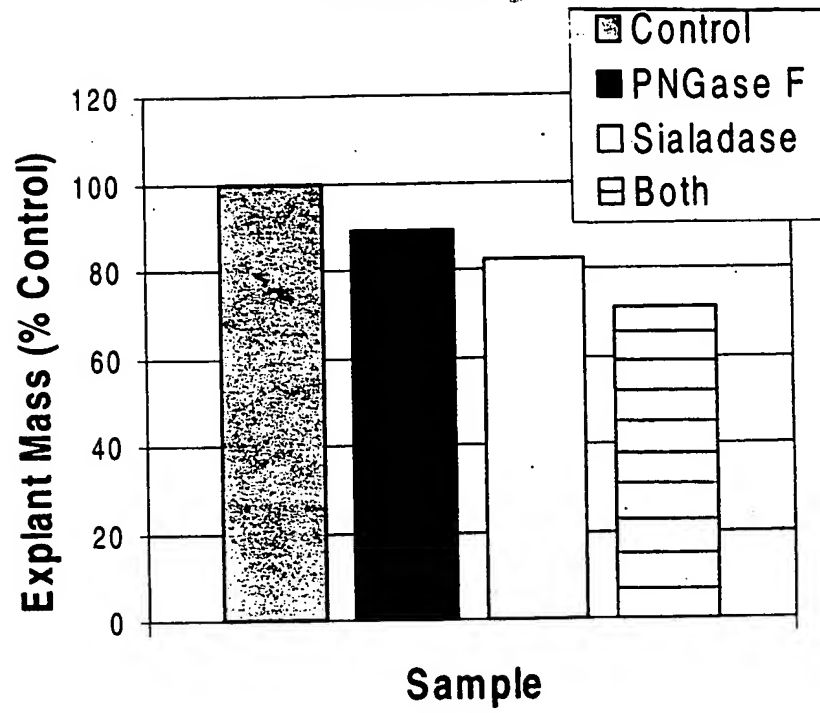


FIGURE 29B

FIGURE 30

Antibody Information

| Specificity | Antigen | Host Species | PC/MC | Source | Catalog No. |
|----------------------------|---------|--------------|------------|--------------------------|-------------|
| TGF- β 1 (human) | Protein | Rabbit | Polyclonal | Promega | G1221 |
| TGF- β 2 (human) | Peptide | Rabbit | Polyclonal | Santa Cruz Biotechnology | sc-90 |
| TGF- β 3 (human) | Peptide | Rabbit | Polyclonal | Santa Cruz Biotechnology | sc-82 |
| BMP-2 (human) | Protein | Rabbit | Polyclonal | Austral Biologics | PA-513-9 |
| BMP-3 (human) | Peptide | Chicken | Polyclonal | Research Genetics | NA |
| BMP-4 (human) | Peptide | Goat | Polyclonal | Santa Cruz Biotechnology | sc-6896 |
| BMP-5 (human) | Peptide | Goat | Polyclonal | Santa Cruz Biotechnology | sc-7405 |
| BMP-6 (human) | Peptide | Mouse | Monoclonal | Novocastra Laboratories | NCL-BMP6 |
| BMP-7 (human) | Peptide | Rabbit | Polyclonal | Research Genetics | NA |
| FGF-1 (human) | Peptide | Goat | Polyclonal | Santa Cruz Biotechnology | sc-1884 |
| osteonectin (bovine) | Protein | Mouse | Monoclonal | DSHB | AON-1 |
| osteocalcin (bovine) | Protein | Rabbit | Polyclonal | Accurate Chemicals | A761/R1H |
| serum albumin (bovine) | Protein | Rabbit | Polyclonal | Chemicon International | AB870 |
| transferrin (human) | Protein | Chicken | Polyclonal | Chemicon International | AB797 |
| apo-A1 lipoprotein (human) | Protein | Goat | Polyclonal | Chemicon International | AB740 |

Figure 31A. Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments

| Band | Sample | Sequence Data | Best Database Match | Match | Identification | Species | Acc. No. | AAs |
|------|-------------------|--------------------------|---------------------------|-------|--|---------|------------------------|-------------|
| 1 | | | | | | | | |
| 2 | fx 49 (1579) | XLAAAGYDVEK | ALAAAGYDVEK | 11/11 | histone H1.c | human | 87668 (NCBI) | 65-75 |
| 3 | fx 67 (1346) | SLEKVCADLIR | SLEKVCADLIR | 11/11 | 40s Ribosomal Protein S20 | rat | R3RT20 (PIR) | 31-41 |
| 4 | fx 65 0 | (V)VCGMLGFPSEAPV | VVCGMLGFPGEKRV | 11/14 | LORP | mouse | AAC95338 (NCBI) | 213- 226 |
| 5 | N terminal seq | STGVLLPLQNNELPG | STGVLLPLQNNELPG | 15/15 | BMP-3 | human | 4557371 (NCBI) | 290- 304 |
| | fx 72 (3925) | STGVLLPLQNNELPGA EYQY | STGVLLPLQNNELPGA AEYQY | 20/20 | BMP-3 | human | 4557371 (NCBI) | 290- 309 |
| | fx 74 (3409) | STGVLLPLQ | STGVLLPLQ | 9/9 | BMP-3 | human | 4557371 (NCBI) | 290- 298 |
| 6 | fx 55 (1566) | (S)QTLQFXE | SQTLQFDE | 7/8 | BMP-3 | human | 4557371 (NCBI) | 346- 353 |
| | fx 47 | VYAF | no match | | ??? | | | |
| | N terminal seq | HAGKYSREKNT(P)A(P) | HGGKYSREKNQPKP | 11/14 | α 2-Macroglobulin Receptor Assoc. Pro. | human | P30533 (Swiss-Prot) | 31-46 |
| | fx 57 (1438) | SQTLQFDEQ | SQTLQFDEQ | 9/9 | BMP-3 | human | 4557371 (NCBI) | 346- 354 |
| | fx 57 (1652) | SLKPSNHA | SLKPSNHA | 8/8 | BMP-3 | human | 4557371 (NCBI) | 410- 417 |
| 7 | fx 51 (1093) | AALRPLVKP | AALRPLVKP | 9/9 | 60s Ribosomal Protein L32 | mouse | P17932 (Swiss-Prot) | 1-9 |
| | fx 37 (no MS) | A(H)I(Q)VERYV | AIVER | 5/5 | 60s Ribosomal Protein L32 | mouse | P17932 (Swiss-Prot) | 109- 113 |
| | fx 37 (no MS) | A(H)I(Q)VERYV | HQSDRYV | 5/7 | 60s Ribosomal Protein L32 | mouse | P17932 (Swiss-Prot) | 22-28 |
| 8 | fx 78 0 | XALF(G)AQLGXALGPI | no match | | ??? | | | |
| 9 | fx 56 (1567) | SQTLQFDEQT | SQTLQFDEQT | 10/10 | BMP-3 | human | P12645 (Swiss-Prot) | 346- 355 |

Figure 31B. Identification of Proteins by Amino Acid Sequencing of Tryptic Fragments

| Band | Sample | Sequence Data | Best Database Match | Match | Identification | Species | Acc. No. | AAs |
|------|---------------------|----------------|---------------------|-------|--------------------------|---------|------------------------|-------------|
| 11 | fx 55 (1311) | SQTLXF | SQTLQF | 5/6 | BMP-3 | human | 4557371 (NCBI) | 346- 351 |
| | fx 47 (1772) | VLATVTKPVGGDK | VLATVTKPVGGDK | 13/13 | 60s Ribosomal Protein L6 | human | Q02878 (Swiss-Prot) | 87-99 |
| | fx 76 (1795) | xVFAL | VFAL | 4/4 | 60s Ribosomal Protein L6 | human | Q02878 (Swiss-Prot) | 273- 276 |
| | fx 61 (1145) | AVPQLQGYLR | AIPQLQGYLR | 9/10 | 60s Ribosomal Protein L6 | human | Q02878 (Swiss-Prot) | 262- 271 |
| 18 | | | | | | | | |
| 22 | fx 58 (1101) | ALDAAYCFR | ALDAAYCFR | 9/9 | TGF- β 2 | human | P08112 (Swiss-Prot) | 303- 311 |
| | fx 69 (no match) | GYNANFCAGACPYL | GYNANFCAGACPYL | 14/14 | TGF- β 2 | human | P08112 (Swiss-Prot) | 340- 353 |
| | fx 66 (1411.71) | VNSQSLSPY | VNSQSLSPY | 9/9 | SPP24 | bovine | Q27967 (Swiss-Prot) | 42-50 |
| 25 | fx 39 (1470) | KAAKPSV(P) | KAAKPSVP | 8/8 | Histone H1.x | human | JC4928 (PIR) | 199- 206 |
| 29 | | | | | | | | |

fx = fraction number (molecular weight of fragment, as measured by SDS-PAGE)

Figure32A. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

| Band | Mass Spec Profile | Species | Acc. No. | Mass Spec Data | Mass Spec Database | Mass Difference | AAs | % Coverage | Comments |
|------|-------------------------------------|---------|-----------------------|----------------|--------------------|-----------------|---------|------------|--|
| 1 | 4 peaks match with histone H1.c | human | 87668 (NCBI) | 1172.97 | 1172.37 | 0.60 | 110-121 | 22 | 15 MS peaks match with Band 2 |
| | | | | 1579.87 | 1579.71 | 0.16 | 65-79 | | |
| | | | | 1708.47 | 1707.89 | 0.58 | 64-79 | | |
| | | | | 2011.58 | 2012.32 | -0.74 | 35-54 | | |
| 2 | 3 peaks match with histone H1.c | human | 87668 (NCBI) | 1579.76 | 1579.71 | 0.05 | 65-79* | 16 | identification of starred peptide confirmed by sequence analysis |
| | | | | 1708.02 | 1707.89 | 0.13 | 64-79 | | |
| | | | | 2012.12 | 2012.32 | -0.20 | 35-54 | | |
| | | | | | | | | | |
| 3 | 7 peaks match with ribosome S20 | rat | R3RT20 (PIR) | 1129.76 | 1129.40 | 0.36 | 50-59 | 62 | 15 MS peaks match with Band 1 |
| | | | | 1156.21 | 1156.30 | -0.09 | 76-83 | | |
| | | | | 1334.46 | 1334.62 | -0.16 | 56-66 | | |
| | | | | 1352.13 | 1351.58 | 0.55 | 88-99 | | |
| | | | | 1518.04 | 1517.77 | 0.27 | 9-21 | | |
| | | | | 1919.02 | 1919.19 | -0.17 | 5-21 | | |
| | | | | 3404.02 | 3404.87 | -0.85 | 88-119 | | |
| | | | | 1987.95 | 1988.27 | -0.32 | 150-167 | | |
| 4 | 3 peaks match with Lysyl Oxidase RP | human | NP002309 (Swiss-Prot) | 2410.35 | 2410.63 | -0.28 | 648-669 | 8 | 12 MS peaks match with Band 8 |
| | | | | 2610.57 | 2610.10 | 0.47 | 455-478 | | |
| | | | | | | | | | |

Figure 32B. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

| Band | Mass Spec Profile | Species | Acc. No. | Mass Spec Data | Mass Spec Database | Mass Difference | AAs | % Coverage | Comments |
|------|---|---------|---------------------|----------------|--------------------|-----------------|----------|------------|---|
| 5 | 9 peaks match with BMP-3 | human | 4557371 (NCBI) | 1113.32 | 1113.31 | 0.01 | 361-368 | 48 | % coverage calculation is relative to the mature BMP-3, 183 AAs (290-472) |
| | | | | 1438.53 | 1438.58 | -0.05 | 346-357 | | |
| | | | | 1566.76 | 1566.76 | 0.00 | 345-357 | | |
| | | | | 1651.86 | 1651.91 | -0.05 | 410-424 | | |
| | | | | 1794.09 | 1794.02 | 0.07 | 346-360 | 17 | identification of starred peptide confirmed by sequence analysis |
| | | | | 2268.46 | 2268.63 | -0.17 | 374-392 | | |
| | | | | 2424.45 | 2424.81 | -0.36 | 373-392 | | |
| 6 | 3 peaks match with α 2-Macroglobulin RAP | human | P30533 (Swiss-Prot) | 3409.15 | 3407.77 | 1.38 | 290-318* | 15 | % coverage calculation is relative to the mature BMP-3, 183 AAs (290-472) |
| | | | | 1002.24 | 1002.15 | 0.09 | 283-290 | | |
| | | | | 2362.58 | 2362.43 | 0.15 | 129-150 | | |
| | | | | 3048.51 | 3048.52 | -0.01 | 257-282 | 15 | % coverage calculation is relative to the mature BMP-3, 183 AAs (290-472) |
| | | | | 1566.93 | 1566.75 | 0.18 | 346-357 | | |
| | | | | 1651.88 | 1651.91 | -0.03 | 410-424 | | |

Figure 32C. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

| Band | Mass Spec Profile | Species | Acc. No. | Mass Spec Data | Mass Spec Database | Mass Difference | AAs | % Coverage | Comments |
|------|--------------------------------------|---------|-----------------------|----------------|--------------------|-----------------|---------|------------|---|
| 7 | 4 peaks match with ribosome L32 | mouse | P17932 (Swiss-Prot) | 1033.25 | 1033.17 | 0.08 | 67-75 | 33 | |
| | | | | 1093.31 | 1093.40 | -0.09 | 1-10* | | |
| | | | | 1134.72 | 1134.28 | 0.44 | 65-74 | | |
| | | | | 1449.78 | 1449.66 | 0.12 | 19-29 | | |
| | 5 peaks match with BMP-3 | human | 4557371 (NCBI) | 1060.42 | 1060.20 | 0.22 | 102-111 | 21 | % coverage calculation is relative to the mature BMP-3, 183 AAs (290-472) |
| 8 | 1 peak matches with Lysyl Oxidase RP | human | NP002309 (Swiss-Prot) | 1113.39 | 1113.31 | 0.08 | 361-368 | 3 | 12 MS peaks match with Band 4 |
| | | | | 1360.26 | 1360.58 | -0.32 | 190-200 | | |
| | | | | 1652.28 | 1651.91 | 0.37 | 410-424 | | |
| | | | | 1793.62 | 1794.02 | -0.40 | 346-360 | | |
| | | | | 2410.37 | 2410.63 | -0.26 | 648-669 | | |
| 9 | 6 peaks match with BMP-3 | human | 4557371 (NCBI) | 1113.14 | 1113.31 | -0.17 | 361-368 | 36 | % coverage calculation is relative to the mature BMP-3, 183 AAs (290-472) |
| | | | | 1438.60 | 1438.58 | 0.02 | 346-357 | | |
| | | | | 1566.77 | 1566.76 | 0.01 | 345-357 | | |
| | | | | 1651.91 | 1651.61 | 0.30 | 410-424 | | |
| | | | | 2901.67 | 2901.19 | 0.48 | 41-66 | | |
| | | | | 3408.94 | 3407.77 | 1.17 | 290-318 | | |

Figure 32 D. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

| Band | Mass Spec Profile | Species | Acc. No. | Mass Spec Data | Mass Spec Database | Mass Difference | AAS | % Coverage | Comments |
|------|-----------------------------------|---------|---------------------|----------------|--------------------|-----------------|---------|------------|---|
| 11 | 5 peaks match with BMP-3 | human | 4557371 (NCBI) | 1113.23 | 1113.31 | -0.08 | 361-368 | 48 | % coverage calculation is relative to the mature BMP-3, 183 AAS (290-472) |
| | | | | 1651.73 | 1651.91 | -0.18 | 410-424 | | |
| | | | | 1793.58 | 1794.02 | -0.44 | 346-360 | | |
| | | | | 2424.24 | 2424.81 | -0.57 | 373-392 | | |
| | | | | 3408.34 | 3407.77 | 0.57 | 290-318 | | |
| | | | | 1140.38 | 1140.23 | 0.15 | 114-122 | | |
| 18 | 5 peaks match with ribosome L6 | human | Q02878 (Swiss-Prot) | 1526.88 | 1526.86 | 0.02 | 141-155 | 16 | |
| | | | | 1059.15 | 1059.12 | 0.03 | 10-20 | | |
| | | mouse | P47911 (Swiss-Prot) | 1145.36 | 1145.35 | 0.01 | 262-271 | | |
| | | | | 1386.74 | 1386.68 | 0.06 | 260-271 | | |
| | | | | 1101.20 | 1101.26 | -0.06 | 303-311 | | |
| | | | | 1175.26 | 1175.42 | -0.16 | 400-409 | | |
| | 4 peaks match with TGF- β 2 | human | P08112 (Swiss-Prot) | 2240.37 | 2240.60 | -0.23 | 312-328 | 52 | |
| | | | | 2691.70 | 2691.91 | -0.21 | 340-362 | | |
| | | | | 1410.93 | 1411.60 | -0.67 | 42-53 | | |
| | | | | 1447.59 | 1447.65 | -0.06 | 113-124 | | |
| | | | | 1540.64 | 1540.60 | 0.04 | 86-98 | | |
| | | | | 1869.10 | 1869.05 | 0.05 | 62-77 | | |
| | 5 peaks match with SPP24 | bovine | Q27967 (Swiss-Prot) | 2268.47 | 2268.57 | -0.10 | 33-53 | 30 | |
| | | | | | | | | | |
| | | | | | | | | | |

Figure32 E. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

| Band | Mass Spec Profile | Species | Acc. No. | Mass Spec Data | Mass Spec Database | Mass Difference | AAS | % Coverage | Comments |
|------|---------------------------------|---------|---------------------|----------------|--------------------|-----------------|---------|------------|---|
| 22 | 5 peaks match with TGF-β2 | human | P08112 (Swiss-Prot) | 1101.15 | 1101.26 | -0.11 | 303-311 | 63 | |
| | | | | 1175.13 | 1175.42 | -0.29 | 400-409 | | |
| | | | | 2084.16 | 2084.42 | -0.26 | 312-347 | | |
| | | | | 2240.25 | 2240.60 | -0.35 | 312-328 | | |
| | | | | 2691.61 | 2691.91 | -0.30 | 340-362 | | |
| | 2 peaks match with SPP24 | bovine | Q27967 (Swiss-Prot) | 1411.23 | 1411.60 | -0.37 | 42-53 | 11 | |
| | | | | 1447.40 | 1447.65 | -0.25 | 113-124 | | |
| | | | | 1208.46 | 1208.40 | 0.06 | 48-57 | | |
| | | | | | | | | | |
| | | | | | | | | | |
| 25 | 5 peaks match with histone H1.x | human | JC4928 (PIR) | 1221.71 | 1222.35 | -0.64 | 107-118 | 14 | |
| | | | | 1349.85 | 1350.52 | -0.67 | 107-119 | | |
| | | | | 1364.57 | 1364.59 | -0.02 | 48-58 | | |
| | | | | 1732.23 | 1732.97 | -0.74 | 43-57 | | |
| | | | | 1060.43 | 1060.20 | 0.23 | 102-111 | | |
| | | | | | | | | | |
| | | | | 1438.83 | 1438.58 | 0.25 | 346-357 | | |
| | | | | 1566.92 | 1566.76 | 0.16 | 345-357 | | |
| | | | | 1651.80 | 1651.91 | -0.11 | 410-424 | | |
| | | | | 3408.86 | 3407.77 | 1.09 | 290-318 | | |
| | 5 peaks match with BMP-3 | human | 4557371 (NCBI) | | | | | 31 | % coverage calculation is relative to the mature BMP-3, 183 AAS (290-472) |

Figure32F. Identification of Proteins by Mass Spectrometry of Tryptic Fragments

| Band | Mass Spec Profile | Species | Acc. No. | Mass Spec Data | Mass Spec Database | Mass Difference | AAs | % Coverage | Comments |
|------|--------------------------|---------|----------------|----------------|--------------------|-----------------|---------|------------|---|
| 29 | 4 peaks match with BMP-3 | human | 4557371 (NCBI) | 1113.22 | 1113.31 | -0.09 | 361-368 | 27 | % coverage calculation is relative to the mature BMP-3, 183 AAs (290-472) |
| | | | | 1438.70 | 1438.58 | 0.12 | 346-357 | | |
| | | | | 1566.86 | 1566.75 | 0.11 | 345-357 | | |
| | | | | 3409.04 | 3407.77 | 1.27 | 290-318 | | |

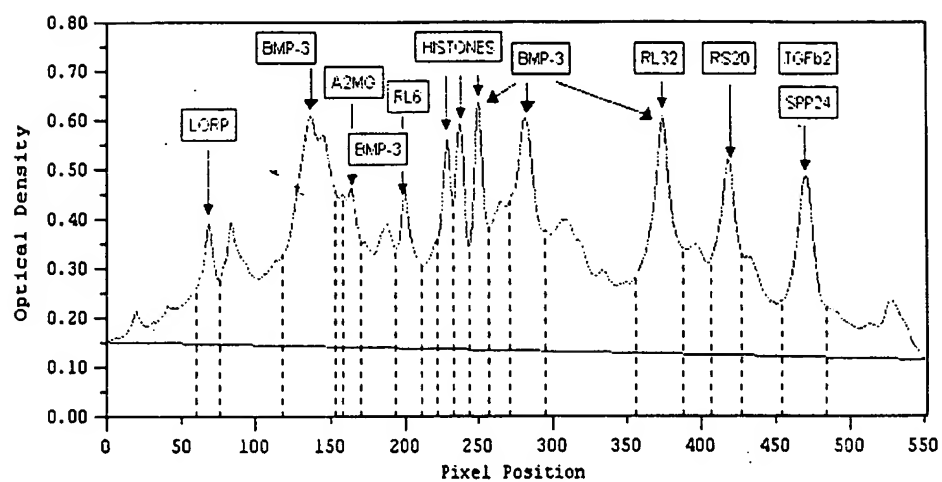


FIGURE 33A



FIGURE 33B

Figure 34. Quantitation of Identified BP proteins

| Identified Protein | Percentage of Total Protein |
|------------------------|-----------------------------|
| LORP | 2 |
| BMP-3 | 11 |
| BMPO3 & A2-MG | 3 |
| RL6 & BMP-3 | 4 |
| Histone | 3 |
| Histone | 3 |
| Histone & BMP-3 | 4 |
| BMP-3 | 8 |
| RL32 & BMP-3 | 8 |
| RS20 | 5 |
| SPP24 & TGF- β 2 | 6 |
| Total | 58% |